







PR 21-APR-1998; 98US-0082614.  
 PR 23-NOV-1998; 98US-0109732.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Cohen D., Blumenfeld M., Chumakov I.;  
 XX  
 DR WPI: 2000 013567/01.  
 XX  
 PT Novel biallelic markers used to construct a high density disequilibrium map of the human genome  
 XX  
 PS claim 1; Page 45B, 2745pp; English.  
 XX  
 CC AAZ5654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences AAZ65579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses; they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B Tho, SFQ 10 NOS 2852, 2913, 2974, 3015, 3096, 3157, 3227, 3297  
 CC and 3367, are not actually given a sequence in the Sequence Listing from the present invention.  
 XX  
 SQ Sequence 47 RP: 12 A; 9 C; 8 G; 18 T; 0 Other;  
 Query Match 0 8%; Score 24.8, DB 21, Length 47,  
 Best Local Similarity 72.7%; Pred. No. 4e-03;  
 Matches 32, Conservative 0; Mismatches 12, Indels 0, Gaps 0;  
 Qy 2664 GATTATCAACCCTTAAGAACTAAGATGAGATAGAG 2707  
 Db 4 GATTATTCCTCTTCTTAAATGAGATGAGATAGAG 47  
 RESULT 7  
 AAL28761  
 ID AAL28761 standard; DNA; 51 BP.  
 AC AAL28761,  
 XX DT 24-JAN-2002 (first entry)  
 XX DF Human SNP oligonucleotide #1989.  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroproactive; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; anionprotein; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytosine; kinase; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX OS Homo sapiens.  
 XX PN WO200147944-A2.  
 XX PD 05-JUL-2001.  
 XX PR 28-DEC-2000; 2000WO-US35498.  
 XX PR 28-DEC-1999; 99US-0173419.  
 XX PR 27-DIC-2000; 2000US-0173419.  
 PA (CURA- ) CURAGEN CORP.

XX PI Shimkets RA, Leach M;  
 XX DR WPI: 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -  
 XX  
 PS Claim 1; Page 1944; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amyloses, amyloid proteins, anionprotein, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, cyclin, polymerase, oncogenes, G-protein coupled receptors and interleukins, interferons, interleukins, kinases, cyclin, polymerase, oncogenes, cytokines, cyclin, polymerase, oncogenes, G-protein coupled receptors and interleukins. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.  
 XX  
 SO Sequence 51 BP: 22 A; 8 C; 9 G; 12 T; 0 other;  
 Query Match 0 8%; Score 24.6; DB 22; Length 51;  
 Best Local Similarity 70.2%; Pred. No. 4.8e+03;  
 Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 Qy 2106 ATTCCGAGAACACATGATGAGAAAGCATAAACATCAAATA 2152  
 Db 5 ATTGGAGGAAAAGAGATGATTCAGATAGATGAAATA 51  
 RESULT 8  
 ABN35766  
 ID ABN35766 standard; DNA; 60 BP.  
 XX  
 AC ABN35766;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE Human spliced transcript detection oligonucleotide SEQ ID No:8514.  
 XX KW Human, mouse, rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss  
 XX OS Homo sapiens.  
 XX PN WO200210444-A2.  
 XX PH 07-FEB-2002.  
 XX PF 20-JUL-2001; 2001WO-1B01903.  
 XX PR 28-JUL-2001; 2001WO-221607P.  
 PR 02-MAY-2001; 2001US-287724P.  
 PA (COMP-) COMPUGEN INC.  
 XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX DP WPI: 2002-257383/30.  
 XX PR New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes -

**Example 1:** SEQ ID 8514 : 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub) transcriptome, where the (sub) transcriptome comprises messenger RNAs transcribed from multiple transcription units that comprise a genome. The library comprises several of oligonucleotide units, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini-libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition. To detect developmental specific genes, and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder, ABN1253 to ABN19589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/putt/published\\_ptt\\_sequences](ftp://wipo.int/putt/published_ptt_sequences).

XX PS Example 1: SEQ ID: 20126; 47pp; English.  
XX the present invention describes oligonucleotide libraries for d-  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC transcriptome comprises messenger RNAs transferred from m-  
CC transcription units that populate a genome. The library consists of  
CC several oligonucleotide ides, each capable of hybridising selectively to  
CC a set of messenger RNAs transferred from a given transcription unit  
CC in the genome, which encodes one or more messenger RNA species. Such  
CC the oligonucleotide ides are useful for detecting mRNAs in biological  
CC samples, in expression profiling studies, in quantitat-  
CC ing the corresponding transcriptome, de-  
CC tecting RNA transcripts and splice variants of human or animal  
CC transcripts. The libraries may also be used as specialised m-  
CC libraries to detect transcripts of a sub-transcriptome, in order to  
CC particular biological or pathological states, and so allowing the  
CC detection of tissue and pathology specific genes such as those  
CC only expressed in specific tissue under a specific pathological  
CC condition, to detect developmental specific genes, and to detect  
CC transcripts and splice variants of a transcriptome of a patient  
CC from a particular disorder. ABN21263 to ABN21269 represent  
CC oligonucleotide sequences from rats, humans and mice, which are  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the  
CC specification, but was obtained in electronic format directly at  
CC <http://wipo.int/patentpublished/patsequences>

RESULT	10			
AHN40943	0			
ID	ABN40			
XX	ABN40			
AC	ABN40			
XX	ABN40			
DT	15-JU			
XX	ABN40			
DE	Human			
XX	Human			
KW	soil			
KW	soil			

XX		Homo sapiens.
XX		OS
XX		WU26021344; A2.
PN		
XX		
PID	07 FEB 2002,	
XX		
IPF	20 JUN 2001;	2001W6 1B01904.
XX		
JIT	28 JUN 2001;	2000W5 221607P.
PR	02 MAY 2001;	200105 287724P.
XX		
PA	(CMMI ) COMGEN INC.	
XX		
F1	shestan, A., Wasserman, A., Mintz, E., Mintz, L., Frajter, S.,	
XX		
WP1	2002 27 084/40.	
XX		
PT	Now oligonucleotide libraries comprising oligonucleotides which	
PT	selectively hybridize to mRNAs transcribed from a transcription unit or	
PT	a genome, useful for detecting tissue pathology, and	
PT	developmental specific genes.	

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**XX** Example 1: SEQ ID 8799; 47pp; English.  
**PS** The present invention describes oligonucleotide libraries for detecting  
**XX** messenger RNAs that populate a (sub-) transcriptome, where the  
**CC** (sub-) transcriptome comprises messenger RNAs transcribed from multiple  
**CC** transcription units that populate a genome. The library comprises  
**CC** several sets of oligonucleotides, each capable of hybridising selectively to a  
**CC** set of messenger RNAs transcribed from a given transcription unit of  
**CC** the genome, which encodes one or more messenger RNA splice variants.  
**CC** The oligonucleotide libraries are useful for detecting mRNAs from a  
**CC** biological sample, in expression profiling studies, in quantitative or  
**CC** quantitative characterising the corresponding transcriptome, and in  
**CC** detecting RNA transcripts and splice variants of human or animal  
**CC** transcriptomes. The libraries may also be used as specialised mini-  
**CC** libraries to detect transcripts of a sub-transcriptome under a  
**CC** particular biological or pathological state, and so allowing the  
**CC** detection of tissue and pathology specific genes such as those genes  
**CC** only expressed in specific tissue and pathological specimens such as those genes  
**CC** only expressed in specific tissue under a specific pathological  
**CC** condition, to detect developmental specific genes, and to detect RNA  
**CC** transcripts and splice variants of a transcriptome of a patient suffering  
**CC** from a particular disorder. ABR27253 to ABN5589 represent  
**CC** oligonucleotide sequences from rats, humans and mice, which are used in  
**CC** the exemplification of the present invention.  
**CC** N.B. The sequence data for this patent did not form part of the printed  
**CC** specification, but was obtained in electronic format directly from WIPO  
**CC** at the website <http://www.wipo.int/patdb/published.jsp?seqid=ABN5589>.

**XX** Sequence 60 bp; 14 A; 10 C; 18 G; 18 T; 0 other;  
**SG** Query Match: 0.88; Score: 22,8; DB: 24; Length: 6,9;  
**Best Local Similarity**: 66.9%; Prod. No.: 1-BE04;  
**Matches**: 46; Conservatives: 0; Mismatches: 17; Indels: 0; gaps: 0;  
**AC**: AHN42702;  
**XX** DT: 14 JUL 2002 (first entry)  
**XX** DE: Human spliced transcript detection oligonucleotide SEQ ID No. 15450.  
**XX** KW: Human; mouse; rat; splice transcript; detection; RNA transcript;  
**KW** splice variant; transcript; oligonucleotide library; ss.  
**XX** OS: Homo sapiens.  
**XX** IN: WO 2002 0449 A2.  
**XX** PD: 07 FEB 2002.  
**XX** PN: WO020449A2.  
**PP** 20 JUL 2001; 2001WO1001901.  
**XX** ID: 09 MAY 1996.  
**PR** 28 JUL 2000; 2000US221607P.  
**IPR** 02 MAY 2001; 2001US287724P.  
**XX** PA: (OMP ) COMGEN INC.  
**XX** PI: Shoshan A, Wasserman A, Mintz E, Mintz L, Faigier S;  
**XX** DR: 2002 2578140.  
**FT** New oligonucleotide libraries comprising oligonucleotides which  
**FT** selectively hybridize to mRNAs transcribed from a transcription unit of  
**FT** a genome, useful for detecting tissue-, pathology-, and  
**FT** developmental specific genes -

**XX** Example 1, SEQ ID 15450; 47pp; English.

**XX** The present invention describes oligonucleotide libraries for detecting  
**CC** messenger RNAs that populate a (sub-) transcriptome, where the  
**CC** (sub-) transcriptome comprises messenger RNAs transcribed from multiple  
**CC** transcription units that populate a genome. The library comprises  
**CC** several sets of oligonucleotides, each capable of hybridising selectively to a  
**CC** set of messenger RNAs transcribed from a given transcription unit of  
**CC** the genome, which encodes one or more messenger RNA splice variants.  
**CC** The oligonucleotide libraries are useful for detecting mRNAs from a  
**CC** biological sample, in expression profiling studies, in quantitative or  
**CC** quantitative characterising the corresponding transcriptome, and in  
**CC** detecting RNA transcripts and splice variants of human or animal  
**CC** transcriptomes. The libraries may also be used as specialised mini-  
**CC** libraries to detect transcripts of a sub-transcriptome under a  
**CC** particular biological or pathological state, and so allowing the  
**CC** detection of tissue and pathology specific genes such as those genes  
**CC** only expressed in specific tissue under a specific pathological  
**CC** condition, to detect developmental specific genes, and to detect RNA  
**CC** transcripts and splice variants of a transcriptome of a patient suffering  
**CC** from a particular disorder. ABR27253 to ABN5589 represent  
**CC** oligonucleotide sequences from rats, humans and mice, which are used in  
**CC** the exemplification of the present invention.  
**CC** N.B. The sequence data for this patent did not form part of the printed  
**CC** specification, but was obtained in electronic format directly from WIPO  
**CC** at the website <http://www.wipo.int/patdb/published.jsp?seqid=ABN5589>.

**XX** Sequence 60 bp; 18 A; 6 C; 19 G; 17 T; 0 other.  
**SG** Query Match: 0.88; Score: 22,8; DB: 24; Length: 6,9;  
**Best Local Similarity**: 62.1%; Prod. No.: 3-BG004;  
**Matches**: 46; Conservatives: 0; Mismatches: 22; Indels: 0; gaps: 0;  
**AC**: AAT28117;  
**XX** DT: 06 JAN 1997 (first entry)  
**XX** DE: AAT28117 Standard; DNA: 40 bp.  
**XX** ID: AAT28117;  
**AC**: AAT28117;  
**XX** DT: 06 JAN 1997 (first entry)  
**XX** DE: Probe for human collagenase bases 181-142.  
**XX** KW: probe; human; fibroblast; ATGGTCTGAGGAACTTCATGCTCTTCA 1806  
**XX** KW: mRNA preparation; senescent cell; different cell; dividing cell;  
**KW** senescence-related gene; gene expression; non senescent cell; liver fibro-  
**KW** bocyte related lipoplasia; retina; donor tissue; senescent melanocyte;  
**KW** melanin; hypopigmentation; SS.  
**XX** OS: Synthetic.  
**XX** PN: WO9614610 A2.  
**PP** 09 MAY 1996.  
**PR** 24 AUG 1995; 95WO9511240.  
**IPR** 31 OCT 1994; 94US0432420.  
**PA**: (GERO-) GERON CORP.  
**XX** PI: Feng J, Funk W, Hirsch KS, Linsken MJK, Villaverde RA;  
**PI**: West MD;  
**DR** WPI: 1996 251664/25.  
**FT** Identifying, isolating, and regulating senescent related genes

PT useful to ameliorate problems associated with accumulation of  
 PT senescent cells, e.g. age-related lipofuscin accumulation in the  
 PT retina and AIDS

XX Disclosure: Page 40; 135pp; English.

CC AAT2814-T28130 represent probes for known genes, used to verify  
 CC expression of the novel senescent related gene sequences isolated from  
 CC fibroblasts (see AAT28076-T28113 and ANT28131-T28173), using the method of  
 CC the invention. In the method of the invention, mRNA is isolated from a  
 CC senescent cell, and a young quiescent cell, and the mRNAs are amplified  
 CC using primers such as those shown in AAT28044-T28075, in separate  
 CC reaction mixtures. The amplified sequences are then separated by size or  
 CC charge, and the products are analysed to identify a gene from young  
 CC quiescent cells and dividing cells, that is present at a different level  
 CC from senescent cells. To enhance the method even more, it can be  
 CC performed in conjunction with an enhanced differential display (EDD)  
 CC method (an mRNA preparation method) on the fibroblasts. The method can  
 CC be used for the rapid and efficient identification and isolation of  
 CC senescent related genes and gene products, and to detect and distinguish  
 CC between senescent and non-senescent cells. It can also be used to  
 CC destroy cells expressing senescence specific (or related) gene products,  
 CC and to screen for compounds capable of altering gene expression in  
 CC senescent cells. The method can also be used to ameliorate problems  
 CC associated with the accumulation of senescent cells such as age-related  
 CC lipofuscin accumulation in the retina, and in the treatment of AIDS.  
 CC Also, the method can be used to distinguish young cells from senescent  
 CC cells in donor tissue, which is useful in removing senescent melanocytes  
 CC overexpressing melanin which cause hypopigmentation, or liver spots.

XX Sequence 40 BP; 7 A; 10 C; 8 G; 15 T; 0 other;

Query Match 0.8%; Score 22.6; DB 17; Length 40;  
 Best Local Similarity 75.7%; Pred. No. 1.6e+04;  
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0.

QY 203 CAAAGGAAATGATGATGGTGGTGGTGGTGG 2.9  
 Db 37 CAAGGCAAGATGATGGTGGTGGTGGTGG 1

## RESULT 15

ABN46589  
 ID ABN46589 standard; DNA; 60 BP.

XX AC ABN46589;  
 XX ID ABN46589;

XX DT 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide Seq ID NO:19337.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 XX splice variant; transcript; oligonucleotide library; ss.

OS Homo sapiens.  
 XX PN WO200210449-A2;  
 XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-1B01903.

XX PR 28-JUL-2000; 2000US-221607P.  
 PR 02-MAY-2001; 2001US-287724P.

XX PA (COMP-) COMPUGEN INC.  
 XX PI Shoshan A, Wasserman A, Mintz E, Mintz I, Fraigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of

a genome, useful for detecting tissue-, pathology- and  
 developmental-specific genes -

PS Example 1: SEQ ID 19337; 47PP; English.

XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a sub-transcriptome, where the  
 CC (sub-) transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridizing selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcripts. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition, to detect developmental specific genes, and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN7253 to ABN59189 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at [http://wipo.int/pubdb/search.html?query=pub\\_id%3D19337](http://wipo.int/pubdb/search.html?query=pub_id%3D19337)

XX Sequence 60 BP; 16 A; 16 C; 15 G; 13 T; 0 other;

Query Match 0.8%; Score 22.6; DB 24; Length 60;  
 Best Local Similarity 64.2%; Pred. No. 2.1e+04;  
 Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 150 CGAGGGTAGAAGGGCTGACTGGAAACATCACCGCGATAAAACCTGT 202  
 Db 8 CGAGGGTAGAAGGGCTGACTGGAAACATCACCGCGATAAAACCTGT 60

Search completed: April 16, 2003, 22:54:17  
 Job time : 661 secs

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Gencore version 5.1.3

score greater than or equal to the score at the result being predicted, and is derived by analysis of the total score distribution.

ALL INFORMATION

RESULT 1	ARO 6.28.3	ARO 6.28.4	dNA	Virchow	VKA (3.0-7.0 ng/ml)
Locus	Streptococcus	6 from patient	48 bp		
DEFINITION		(IS 5776691)			
ACCESSION	ARO 6.28.3				
VERSION	ARO 6.28.3.1	G1:39/2560			
KEYWORDS					
SOURCE	Unknown				
ORGANISM	Unknown				
	Unclassified				
REFERENCE	1 (bases 1 to 48)				
AUTHORS	Vojdani A. and Mardach E.				
TITLE	Detection of chronic fatigue syndrome by decreased levels of tRNA				
1. Inhibitor of tRNA					
PATENT	US 5776690 A	6,07	IND. 1998		
JOURNAL					

FEATURES location/Qualifiers  
source 1. .48  
BASE COUNT 14 a 11 c 12 q 11 t  
ORIGIN /organism="unknown"

Query Match 0.98; Score 25; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2 5e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
KEYWORDS SOURCE human.

ORGANISM Homo sapiens  
Fukuyama, Metzger, Chardia, Chaitin, Vertebrates, Eutherostomata;  
Mammalia; Eutheria; Primates, Catarhinida, Hominidae; Homo.  
REFERENCE J  
AUTHORS Pyly, P.A., Xu, T. and Sechrist, H.  
TITLE compositions and methods for the therapy and diagnosis of colon  
cancer  
JOURNAL Patent: WO 02122280-A (US)  
CORIXA CORPORATION (US)  
FEATURES Location/Qualifiers  
source 1. .58  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 0 a 8 c 5 g 45 t  
ORIGIN

RESULT 2  
AR064498/C AR064498 Sequence 71 from Patent US 5847096. linear PAT 29-SEP-1999  
LOCUS AR064498  
DEFINITION AR064498  
VERSION AR064498 1  
KEYWORDS SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Schibert, M., Harmsion, G. G., Li, Chen, C.-J. and Banerjee, A.  
TITLE DNA constructs encoding CD4 fusion proteins  
JOURNAL Patent: US 5847096-A 71 08-DEC-1998;  
FEATURES Location/Qualifiers  
source 1. .54  
BASE COUNT 14 a 18 c 10 q 12 t  
ORIGIN /organism="unknown"  
Query Match 0.8%; Score 23; DB 6; Length 54;  
Best Local Similarity 74.4%; Pred. No. 8.4e-05;  
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
KEYWORDS SOURCE  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 59)  
AUTHORS Koetter, P., Entian, K.D. and Diu-Herrrend, A.  
TITLE Method for screening antimycotic substances using essential genes  
JOURNAL Patent: WO 9959607-A 95 04-NOV-1999;  
LOCUS KOETTER PETER (DE); ENTIAN KURT DIETER (DE); DIU HERREND ANITA  
DEFINITION (FR); HOECHST MARION ROUSSEL INC (FR)  
VERSION AR011418  
KEYWORDS Location/Qualifiers  
source 1. .59  
/organism="synthetic construct"  
/db\_xref="taxon:3260"  
/note="primer YDR499w-S1"  
BASE COUNT 16 a 11 c 18 q 14 t  
ORIGIN

Query Match 0.8%; Score 22.4; DB 6; Length 59;  
Best Local Similarity 72.5%; Pred. No. 1.2e+06;  
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
KEYWORDS SOURCE

RESULT 3  
A21609/C A21609 oligonucleotide.  
DEFINITION A21609  
VERSION A21609 1  
KEYWORDS SOURCE synthetic construct.  
ORGANISM synthetic construct.  
FEATURES artificial sequences.  
source 1. .37  
/organism="synthetic construct"  
/db\_xref="taxon:2630"  
BASE COUNT 6 a 5 c 4 q 22 t  
ORIGIN

Query Match 0.8%; Score 22.6; DB 6; Length 37;  
Best Local Similarity 75.7%; Pred. No. 1e+06;  
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
KEYWORDS SOURCE

RESULT 4  
AX381765/C AX381765 Sequence 14 from patent US 6361943.  
LOCUS AX381765 1  
DEFINITION Sequence 14 from patent US 6361943.  
VERSION AR201911  
KEYWORDS SOURCE Unknown.  
ORGANISM Unknown.

me]assisted.

REFERENCE	1 (bases 1 to 60)
AUTHORS	Erhard,K. and Chriithiane,S.
TITLE	Novel Escherichia coli/host vector system based on selection not relying on antibiotic by complementing auxotrophy
JOURNAL	Patent; JP 00050888-A 7 22 FEB 2000;
COMMENT	RCCIE DIAGNOSTICS GMBH
PN	OS Artificial Sequence
FT	JP 2000050888-A/7
PD	22 FEB 2000
PP	15-JUL-1999 JP 1999202303
PR	15-JUL-1998 EP 98113156,8,09-OCT-1998
ERHARD KOPETSUKI, CHRISTIANE SCHANZ	PP 98119078,8 P1
PC	C12N15/09,C12NL21,C12P21/02/(C12N1/21,C12P21/19), C12N15/02
PC	C12R11:19,
CC	C12N15/00
FH	KEY
FT	source
FT	Location/Qualifiers
1..60	/organism="Artificial Sequence".
1..60	/organism="synthetic construct".
19 a	/db_xref="taxon:32630"
14 c	13 g 14 t
FEATURES	Query Match
source	Best Local Similarity 0.8%; Score 22,2; DB 6; Length 60;
BASE COUNT	Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
ORIGIN	QY 1449 GAGGGGAGATGGAAAATGAGGAAGATATTGCCGAAATGTCCTGT 1499
Db	54 GATGATAAGCTGTCAAACATAGGGGGCCATATGGCCCTATAGGCCCTT 4
RESULT	11 AF224157/C
LOCUS	AF224157
DEFINITION	Mus musculus GBTCR10.53 T cell receptor beta-chain mRNA
ACCESION	54 bp linear
VERSION	Partial cds.
KEYWORDS	AP224157
SOURCE	AP224157.1 GI:6959997
ORGANISM	Mus musculus
Fukuyama; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 54)
AUTHORS	Wallace,M.E., Bryden,M., Cose,S.C., Coles,R.M., Schumacher,T.N., Brooks,A. and Carbone,F.R.
TITLE	A bias towards D-element encoded CDR3 sequences in the naive TCR repertoire enhances the CTL response to an immunodominant HSV-1 determinant
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 54)
AUTHORS	Wallace,M.E., Bryden,M., Cose,S.C., Coles,R.M., Schumacher,T.N., Brooks,A. and Carbone,F.R.
TITLE	Submitted (13-JAN-2000) Pathology and Immunology, Monash Medical School, Commercial Rd., Prahran, Victoria 3181, Australia
FEATURES	Location/Qualifiers
source	/organism="Mus musculus" /strain="C57Bl/6J" /db_xref="taxon:10090" /clone="GBTCR10.53" /cell_line="T cell line specific for HSV-1 9B498-505 <1..54 /note="TCRBV10" /codon_start=1 /product="T cell receptor beta-chain CDR3" /protein_id="AAF33104_1"
CDS	<1..54
FT	source

REFERENCE	/db_xref="GI:6959998"
AUTHORS	/transl ign="LCASSWGVYEVFGP;ST"
TITLE	8 a 18 c 16 g 12 t
JOURNAL	BASE COUNT
COMMENT	ORIGIN
PN	Query Match
FT	Best Local Similarity 0.8%; Score 22; DB 10; Length 54;
PD	Matches 28; conservative 0; Mismatches 10; Indels 0; Gaps 0;
PP	QY 1534 GTCCTCGATACCCACAGAATGCAACCAA 1571
PR	Db 39 GTACTGTACATGCCAGGAATGCTGGCACAGA 2
ERHARD KOPETSUKI, CHRISTIANE SCHANZ	RESULT 12
PC	AR151069/c
CC	AR151069
FH	LOCUS
KEY	DEFINITION Sequence 9 from patent US 5231850. DNA
FT	ACCESSION AR151069
FT	VERSION AR151069.1
FT	KEYWORD SOURCE
FT	ORGANISM Unknown
FT	Unclassified
FT	REFERENCE 1 (bases 1 to 39)
FT	AUTHORS Okano,F., Saitoh,M. and Yamada,K.
FT	TITLE Canine interleukin 12
FT	FEATURES patent: US 5231850-A 9 15-MAY-2001;
FT	SOURCE 1..39 /organism="unknown"
FT	BASE COUNT 4 a 14 c 12 q 9 t
FT	Query Match
FT	Best Local Similarity 0.7%; Score 21,8; DB 6; Length 39;
FT	BASE COUNT 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
FT	ACCESSION E15025
FT	VERSION E15025.1 GI:5709708
FT	FEATURES SOURCE
FT	ORGANISM unclassified
FT	REFERENCE 1 (bases 1 to 39)
FT	AUTHORS Okano,F.
FT	TITLE CANINE INTERLEUKIN 12 AND ITS PRODUCTION
FT	JOURNAL PATENT: JP 1998036397-A 9 10-FEB-1998;
FT	COMMENT OS None
FT	OC Artificial sequences
FT	PN JP 1998036397_A/9
FT	FD 10-FEB-1998
FT	PP 08-NOV-1996 JP 1996296789
FT	PR 08-NOV-1995 JP 95p 289729, 23-MAY-1996 JP 96p
FT	OKANO FUMIYOSHI PC CGK14/54,CGTH21/04,C12N5/20,C12N5/04,C12F21/32,(C12N5/10, PC C12R1/91),(C12P21/02,C12R1/91); CC strandedness: Single; CC topology: Linear; Key
FT	FT source 1..39

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo

Mammalia: Eutheria; Primates; Catarrhini; hominidae, homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 6)  
Picoult Newburg, L., and Pohl, M.  
genotyping reagents, kits and methods of use thereof  
Patent No. 0129262-A 1440 26-APR-2001;  
Orchid Biosciences, Inc. (US)

FEATURES	source*	Location/Qualifiers
Zordanism	51	"Homo sapiens"

ASSESSMENT OF THE PRACTICALITY OF THE PROPOSED SYSTEM  
ASSESSMENT OF THE PRACTICALITY OF THE PROPOSED SYSTEM

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Best Match          0.706      pred. No.: 1.7e-06;
Best local similarity 0.7078;  Matches 29; Conservat. 0; Mismatches 12; indels 0; gaps 0;

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Table 4.9 *Actual and potential costs of energy*

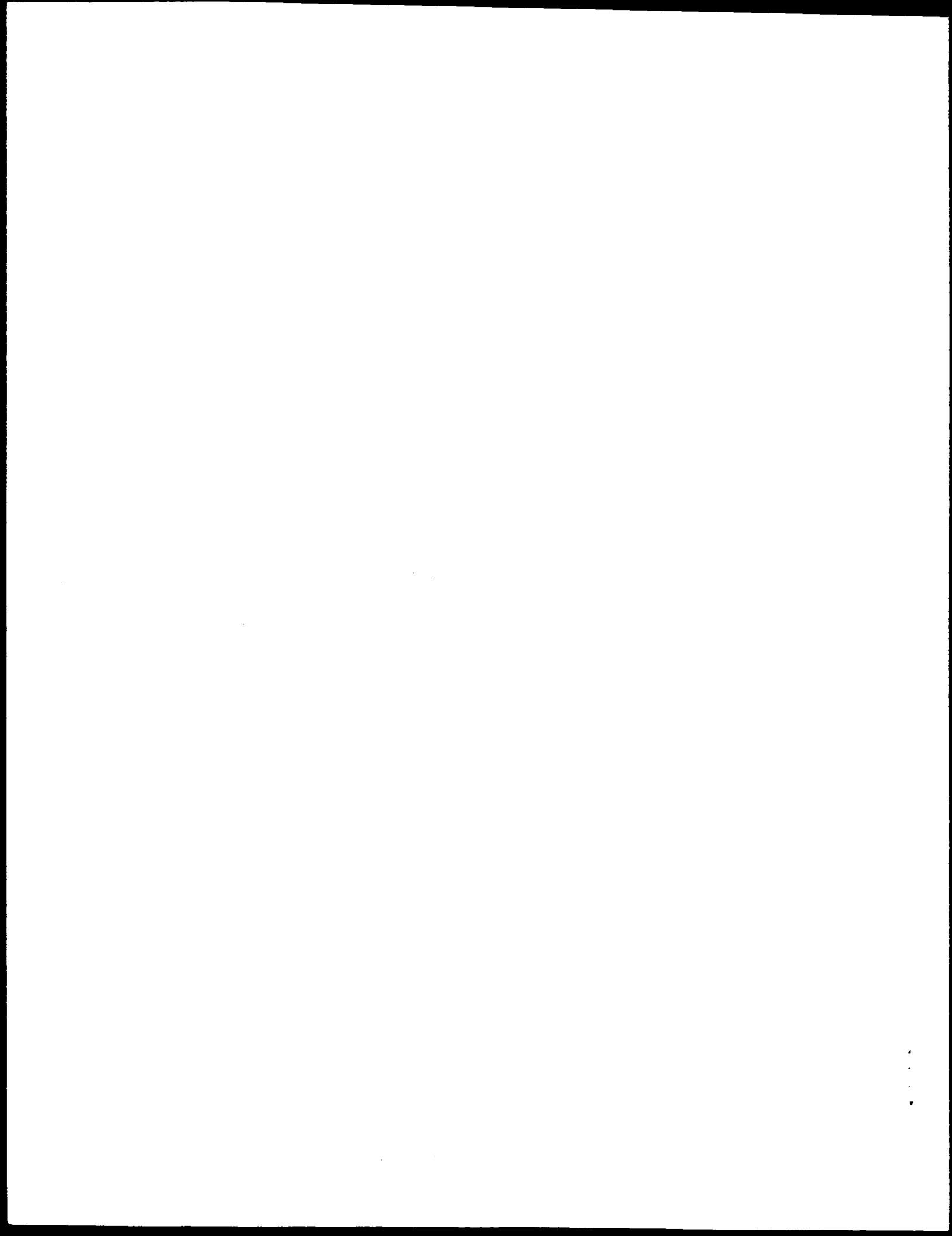
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NAME	AX16544 /c
LOCUS	AX16544.9
DEFINITION	Sequence 644 from Patient W0148586
ACCESSION	AX16544.9
VERSION	AX16544.1
KEYWORDS	G1;14546278
SOURCE	
ORGANISM	human
COMMENT	
FEATURES	
BASE COUNT	51 bp
DNA	W0148586
LINEAR	Linear
PAT	PAT 22 JUN 2001

---

<b>ORGANISM</b>	Homo sapiens
<b>EUKARYOTIC</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
<b>MAMMALIAN</b>	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
<b>REFERENCE</b>	I (bases 1 to 61)
<b>AUTHORS</b>	Shimkets, R. A. and Leach, M.
<b>TITLE</b>	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
<b>PATENT</b>	WO 0138366 A644 31-MAY-2001;
<b>JOURNAL</b>	Curratent Corporation (US)
<b>FEATURES</b>	location/Qualifiers
<b>SOURCES</b>	1 - 51

organism - "Homo sapiens"  
db-refer - "Taxon: 9606"  
26  
26 "single nucleotide polymorphism"



ALIMENTATION

CITY: Washington  
 STATE: D.C.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10-228,070  
 FILING DATE: 27-Aug-2002  
 CLASSIFICATION: (D) REFERENCE: 2002-1108/LC/01416  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 10/046,722  
 FILING DATE: 17-Jan-02  
 APPLICATION NUMBER: 09/284,627  
 FILING DATE: 02-Jun-99  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 60  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Other nucleic acid  
 DESCRIPTION: Synthetic DNA  
 FEATURE:  
 OTHER INFORMATION: has a sequence partly complementary to SEQ ID NO: 17  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-10-228-070-14

Query Match 0.8%; Score 22.4; DB 12; Length 60;  
 Best Local Similarity 65.7%; Pred. No. 1.2e+04;  
 Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 SEQ 2111 GGAGAACACATGATGAAAGCATATAATTAAATT 2158  
 Db 55 GGGAGGTCAAAAAGAAAAAAGAAAAAAAGAAACTAAGG 8

RESULT 4  
 US-09-764-872-151  
 TYPE: nucleic acid  
 Sequence 151, Application US/09764872  
 Publication No. US20030050231A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PA125  
 CURRENT APPLICATION NUMBER: US/09/764,872  
 CURRENT FILING DATE: 2001-01-17  
 PRIOR APPLICATION DATA removed - consult PALM or file wrapper  
 NUMBER OF SEQ ID NO: 957  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 151  
 LENGTH: 51  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-764-872-151

Query Match 0.8%; Score 22.2; DB 9; Length 51;  
 Best Local Similarity 67.1%; Pred. No. 1.2e+04;  
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 SEQ 1750 GGTGGTMAACATTCCTCCAGAAACTAAGG 1784  
 Db 1 GATGTTCTACCTTTTCAGATGAGAAACTAAGG 35

RESULT 5  
 US-08-781-986A-1652/c  
 Sequence 1652, Application US/08781986A  
 Publication No. US20030054436A1  
 GENERAL INFORMATION:  
 APPLICANT: Charles Kunsch  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5255  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10-046,722  
 FILING DATE: 17-Jan-2002  
 CLASSIFICATION: (D) REFERENCE: 2001-1108/LC/01416  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/284,627  
 FILING DATE: 02-Jun-99  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:





Ob 57 GATATTTCAGGAGACAAATGAGCTTAAATTAG; 12

RESULT 14 US 109 414 12/G Sequence 12, Application US/109934

Publication No. US/0040008434A1

GENERAL INFORMATION:

APPLICANT: Woodage, Trevor et al.

TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

PROTEINS, NUCLEAR ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF

FILE REFERENCE: CL000669D1V 3

CURRENT APPLICATION NUMBER: US/10/199, 334

CURRENT FILING DATE: 2002 07 22

PRIORITY APPLICATION NUMBER: 09/609, 816

PRIOR FILING DATE: 2001 03 27

PRIOR APPLICATION NUMBER: 60/192, 408

PRIOR FILING DATE: 2000 03 27

PRIOR APPLICATION NUMBER: 60/212, 725

PRIOR FILING DATE: 2000 06 20

PRIOR APPLICATION NUMBER: 09/609, 816

PRIOR FILING DATE: 2000 07 03

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 57

TYPE: DNA

ORGANISM: Homo sapiens

US 109 414 12

Query Match Score 0.78; Length 57;

Host Local Similarity 65.28; pred. No. 4.4e+04;

Matches 40; conservative 0; Mismatches 16; Index 0;

Caps 0; Other Information: restriction site

US 09 758 017A 18

Sequence 18, Application US/09758017A

Patent No. US/2010557A1

GENERAL INFORMATION:

APPLICANT: Latos, Olav

APPLICANT: Willasen, Niels Peter

APPLICANT: Giddal, Per Henrik

APPLICANT: Gjellevik, Dan Rune

TITLE OF INVENTION: Cod uracil DNA glycosylase, gene coding therefore,

TITLE OF INVENTION: recombinant DNA containing said gene or operative parts

TITLE OF INVENTION: thereof, a method for preparing said protein and the

TITLE OF INVENTION: use of said protein or said operative parts

CURRENT APPLICATION NUMBER: US/09/758,017A

CURRENT FILING DATE: 2001 01 10

PRIORITY APPLICATION NUMBER: 2000 5428

PRIOR FILING DATE: 2000 10 27

PRIOR APPLICATION NUMBER: 2000 01 12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 18

LENGTH: 47

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial sequence: Artificial

OTHER INFORMATION: Sequence - primer used to prepare reading gene

US 09 758 017A 18

Query Match Score 0.78; Length 47;

pred. No. 4.4e+04;

Matches 28;保守性 0; 错配数 0;

Indels 0; 帧移 0;

RESULT 15 US-09-790-417-2-31

Sequence 23, Application US/09790417

Patient No. US/200041470A1

GENERAL INFORMATION:

APPLICANT: Shultz, John W.

APPLICANT: Lewis, Martin K.

APPLICANT: Lachapelle, Daniel

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard B.

APPLICANT: Andrews, Christopher A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Arant

APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

CURRENT APPLICATION NUMBER: US/09/790,417

CURRENT FILING DATE: 2001 02 22

PRIOR APPLICATION NUMBER: 09/758,572

PRIOR FILING DATE: 1999 07 21

PRIOR APPLICATION NUMBER: 09/686H755B8

FILE REFERENCE: Pro-103 686H755B8

NUMBER OF SEQ ID NOS: 290

SOFTWARE: Patent In Ver. 2.0

LENGTH: 51

SEQ ID NO 24

OTHER INFORMATION: description of Artificial sequence: former for first

US-09-790-417-2-31

Query Match Score 0.78; Length 51;

Host Local Similarity 68.38; pred. No. 4.4e+04;

Matches 28;保守性 0; 错配数 0;

Indels 0; 帧移 0;

RESULT 16 US-09-790-417-2-31

Sequence 24, Application US/09790417

Patient No. US/200041470A1

GENERAL INFORMATION:

APPLICANT: Latos, Olav

APPLICANT: Gjellevik, Dan Rune

APPLICANT: Willasen, Niels Peter

APPLICANT: Giddal, Per Henrik

APPLICANT: Gjellevik, Dan Rune

TITLE OF INVENTION: Cod uracil DNA glycosylase, gene coding therefore,

TITLE OF INVENTION: recombinant DNA containing said gene or operative parts

TITLE OF INVENTION: thereof, a method for preparing said protein and the

TITLE OF INVENTION: use of said protein or said operative parts

CURRENT APPLICATION NUMBER: US/09/758,017A

CURRENT FILING DATE: 2001 01 10

PRIORITY APPLICATION NUMBER: 2000 5428

PRIOR FILING DATE: 2000 10 27

PRIOR APPLICATION NUMBER: 2000 01 12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 18

LENGTH: 47

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial sequence: Artificial

OTHER INFORMATION: Sequence - primer used to prepare reading gene

US 09 758 017A 18

Query Match Score 0.78; Length 47;

pred. No. 4.4e+04;

Matches 28;保守性 0; 错配数 0;

Indels 0; 帧移 0;

RESULT 17 US-09-790-417-2-31

Sequence 17, Application US/09790417

Patient No. US/200041470A1

GENERAL INFORMATION:

APPLICANT: Lewis, Martin K.

APPLICANT: Lachapelle, Daniel

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard B.

APPLICANT: Andrews, Christopher A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Arant

APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

CURRENT APPLICATION NUMBER: US/09/790,417

CURRENT FILING DATE: 2001 02 22

PRIOR APPLICATION NUMBER: 09/758,572

PRIOR FILING DATE: 1999 07 21

PRIOR APPLICATION NUMBER: 09/686H755B8

FILE REFERENCE: Pro-103 686H755B8

NUMBER OF SEQ ID NOS: 290

SOFTWARE: Patent In Ver. 2.0

LENGTH: 51

SEQ ID NO 24

OTHER INFORMATION: description of Artificial sequence: former for first

US-09-790-417-2-31

Query Match Score 0.78; Length 51;

Host Local Similarity 68.38; pred. No. 4.4e+04;

Matches 28;保守性 0; 错配数 0;

Indels 0; 帧移 0;

RESULT 18 US-09-790-417-2-31

Sequence 18, Application US/09790417

Patient No. US/200041470A1

GENERAL INFORMATION:

APPLICANT: Lewis, Martin K.

APPLICANT: Lachapelle, Daniel

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard B.

APPLICANT: Andrews, Christopher A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Arant

APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

CURRENT APPLICATION NUMBER: US/09/790,417

CURRENT FILING DATE: 2001 02 22

PRIOR APPLICATION NUMBER: 09/758,572

PRIOR FILING DATE: 1999 07 21

PRIOR APPLICATION NUMBER: 09/686H755B8

FILE REFERENCE: Pro-103 686H755B8

NUMBER OF SEQ ID NOS: 290

SOFTWARE: Patent In Ver. 2.0

LENGTH: 51

SEQ ID NO 24

OTHER INFORMATION: description of Artificial sequence: former for first

US-09-790-417-2-31

Query Match Score 0.78; Length 51;

Host Local Similarity 68.38; pred. No. 4.4e+04;

Matches 28;保守性 0; 错配数 0;

Indels 0; 帧移 0;

RESULT 19 US-09-790-417-2-31

Sequence 19, Application US/09790417

Patient No. US/200041470A1

GENERAL INFORMATION:

APPLICANT: Lewis, Martin K.

APPLICANT: Lachapelle, Daniel

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard B.

APPLICANT: Andrews, Christopher A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Arant

APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

CURRENT APPLICATION NUMBER: US/09/790,417

CURRENT FILING DATE: 2001 02 22

PRIOR APPLICATION NUMBER: 09/758,572

PRIOR FILING DATE: 1999 07 21

PRIOR APPLICATION NUMBER: 09/686H755B8

FILE REFERENCE: Pro-103 686H755B8

NUMBER OF SEQ ID NOS: 290

SOFTWARE: Patent In Ver. 2.0

LENGTH: 51

SEQ ID NO 24

OTHER INFORMATION: description of Artificial sequence: former for first

US-09-790-417-2-31

Query Match Score 0.78; Length 51;

Host Local Similarity 68.38; pred. No. 4.4e+04;

Matches 28;保守性 0; 错配数 0;

Indels 0; 帧移 0;

RESULT 20 US-09-790-417-2-31

Sequence 20, Application US/09790417

Patient No. US/200041470A1

GENERAL INFORMATION:

APPLICANT: Lewis, Martin K.

APPLICANT: Lachapelle, Daniel

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard B.

APPLICANT: Andrews, Christopher A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Arant

APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

CURRENT APPLICATION NUMBER: US/09/790,417

CURRENT FILING DATE: 2001 02 22

PRIOR APPLICATION NUMBER: 09/758,572

PRIOR FILING DATE: 1999 07 21

PRIOR APPLICATION NUMBER: 09/686H755B8

FILE REFERENCE: Pro-103 686H755B8

NUMBER OF SEQ ID NOS: 290

SOFTWARE: Patent In Ver. 2.0

LENGTH: 51

SEQ ID NO 24

OTHER INFORMATION: description of Artificial sequence: former for first

US-09-790-417-2-31

Query Match Score 0.78; Length 51;

Host Local Similarity 68.38; pred. No. 4.4e+04;

Matches 28;保守性 0; 错配数 0;

Indels 0; 帧移 0;

RESULT 21 US-09-790-417-2-31

Sequence 21, Application US/09790417

Patient No. US/200041470A1

GENERAL INFORMATION:

APPLICANT: Lewis, Martin K.

APPLICANT: Lachapelle, Daniel

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard B.

APPLICANT: Andrews, Christopher A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Arant

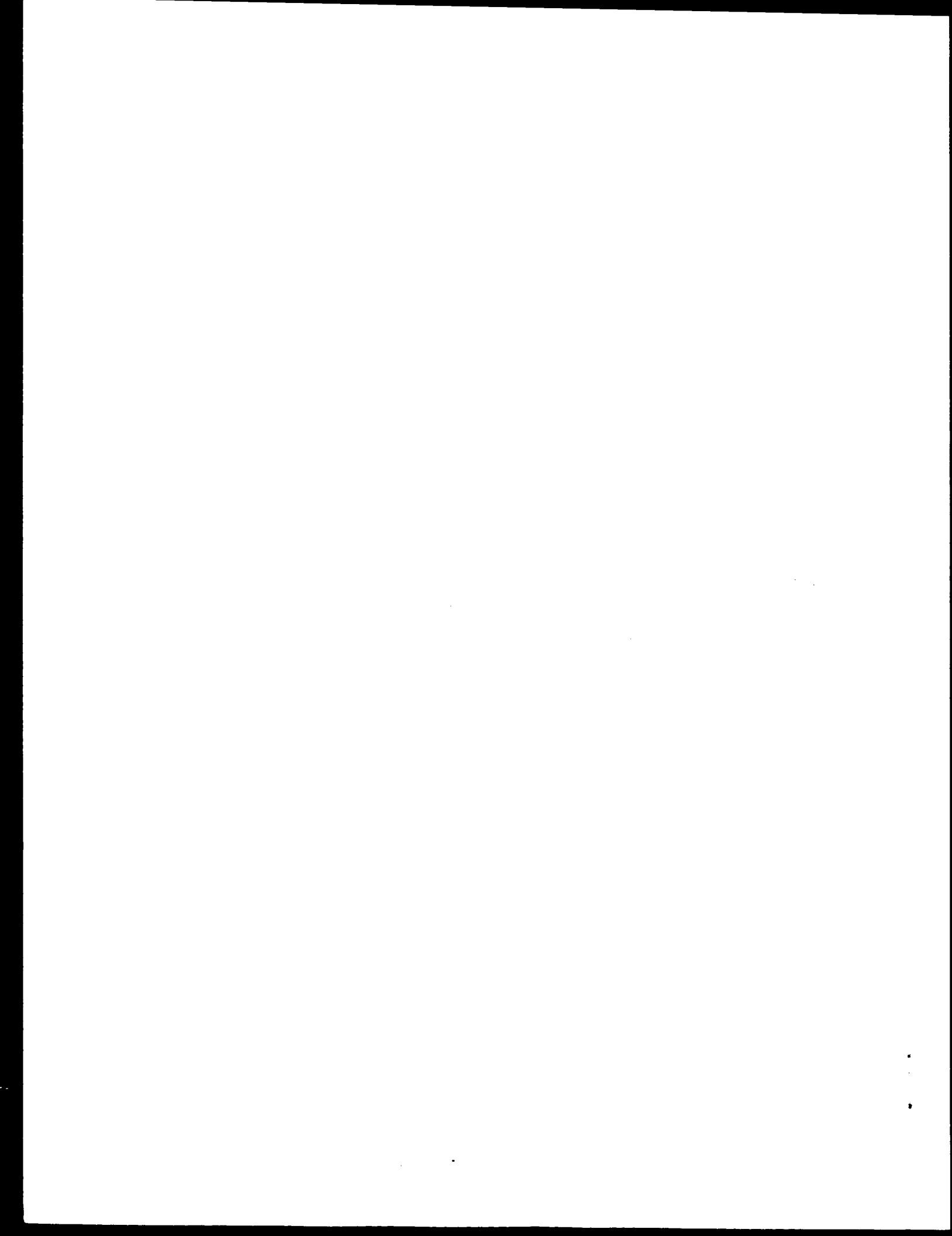
APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

CURRENT APPLICATION NUMBER: US/09/7



Result No.	Score	Query	Match length	OB	ID	Description
1	27.8	em_qss_vrt;*	9	AA417159	AA417159 znt602.1	
2	27.4	em_qss_vrt;*	9	AA524624	A1524624 Tact12.x	
3	26.6	em_qss_vrt;*	9	CRS10V2	AK240521.17 Tact10	
4	25.6	em_qss_vrt;*	9	16592115	AK240521.16 0622054	
5	25.6	em_qss_vrt;*	9	16571284	AK240521.14 1658054	
6	25.2	em_qss_vrt;*	9	16571284	AK240521.13 1658054	
7	24.6	em_qss_vrt;*	9	16571284	AK240521.12 1658054	
8	24.4	em_qss_vrt;*	9	16571284	AK240521.11 1658054	
9	24.2	em_qss_vrt;*	9	16571284	AK240521.10 1658054	
10	24.2	em_qss_vrt;*	9	16571284	AK240521.9 1658054	
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15	23.2	em_qss_vrt;*	9	16571284	AK240521.4 1658054	
16	23.2	em_qss_vrt;*	9	16571284	AK240521.3 1658054	
17	22.6	em_qss_vrt;*	9	16571284	AK240521.2 1658054	
18	22.4	em_qss_vrt;*	9	16571284	AK240521.1 1658054	
19	22.4	em_qss_vrt;*	9	16571284	AK240521.0 1658054	
20	22.4	em_qss_vrt;*	9	16571284	AK240521.9 1658054	
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26	21	em_qss_vrt;*	9	16571284	AK240521.3 1658054	
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29	21.8	em_qss_vrt;*	9	16571284	AK240521.0 1658054	
30	21.8	em_qss_vrt;*	9	16571284	AK240521.9 1658054	
31	21.8	em_qss_vrt;*	9	16571284	AK240521.8 1658054	
32	21.8	em_qss_vrt;*	9	16571284	AK240521.7 1658054	
33	21.8	em_qss_vrt;*	9	16571284	AK240521.6 1658054	
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35	21.6	em_qss_vrt;*	9	16571284	AK240521.4 1658054	
36	21.4	em_qss_vrt;*	9	16571284	AK240521.3 1658054	
37	21.4	em_qss_vrt;*	9	16571284	AK240521.2 1658054	
38	21.4	em_qss_vrt;*	9	16571284	AK240521.1 1658054	
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		1.3: qb_cst4;*	1			
		1.4: qb_cst5;*	1			
		1.5: em_estim;*	1			
		1.6: em_estim;*	1			
		1.7: qb_qss;*	1			
		1.8: em_qss_hum;*	1			
		1.9: em_qss_inv;*	1			
		2.0: em_qss_pfo;*	1			
		2.1: em_qss_vrt;*	1			
		2.2: em_qss_vrt;*	1			
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		2.4: em_qss_inv;*	1			
		2.5: em_qss_other;*	1			
		2.6: em_qss_pfo;*	1			
		2.7: em_qss_vrt;*	1			
		2.8: qb_1lce;*	1			
		2.9: qb_cst3;*	1			
		3.0: qb_cst4;*	1			
		3.1: qb_cst5;*	1			
		3.2: qb_1lce;*	1			
		3.3: qb_cst3;*	1			
		3.4: qb_cst4;*	1			
		3.5: qb_cst5;*	1			
		3.6: qb_1lce;*	1			
		3.7: qb_cst3;*	1			
		3.8: qb_cst4;*	1			
		3.9: qb_cst5;*	1			
		3.10: qb_1lce;*	1			
		3.11: qb_cst3;*	1			
		3.12: qb_cst4;*	1			
		3.13: qb_cst5;*	1			
		3.14: qb_1lce;*	1			
		3.15: qb_cst3;*	1			
		3.16: qb_cst4;*	1			
		3.17: qb_cst5;*	1			
		3.18: qb_1lce;*	1			
		3.19: qb_cst3;*	1			
		3.20: qb_cst4;*	1			
		3.21: qb_cst5;*	1			
		3.22: qb_1lce;*	1			
		3.23: qb_cst3;*	1			
		3.24: qb_cst4;*	1			
		3.25: qb_cst5;*	1			
		3.26: qb_1lce;*	1			
		3.27: qb_cst3;*	1			
		3.28: qb_cst4;*	1			
		3.29: qb_cst5;*	1			
		3.30: qb_1lce;*	1			
		3.31: qb_cst3;*	1			
		3.32: qb_cst4;*	1			
		3.33: qb_cst5;*	1			
		3.34: qb_1lce;*	1			
		3.35: qb_cst3;*	1			
		3.36: qb_cst4;*	1			
		3.37: qb_cst5;*	1			
		3.38: qb_1lce;*	1			
		3.39: qb_cst3;*	1			
		3.40: qb_cst4;*	1			
		3.41: qb_cst5;*	1			
		3.42: qb_1lce;*	1			
		3.43: qb_cst3;*	1			
		3.44: qb_cst4;*	1			
		3.45: qb_cst5;*	1			
		3.46: qb_1lce;*	1			
		3.47: qb_cst3;*	1			
		3.48: qb_cst4;*	1			
		3.49: qb_cst5;*	1			
		3.50: qb_1lce;*	1			
		3.51: qb_cst3;*	1			
		3.52: qb_cst4;*	1			
		3.53: qb_cst5;*	1			
		3.54: qb_1lce;*	1			
		3.55: qb_cst3;*	1			
		3.56: qb_cst4;*	1			
		3.57: qb_cst5;*	1			
		3.58: qb_1lce;*	1			
		3.59: qb_cst3;*	1			
		3.60: qb_cst4;*	1			
		3.61: qb_cst5;*	1			
		3.62: qb_1lce;*	1			
		3.63: qb_cst3;*	1			
		3.64: qb_cst4;*	1			
		3.65: qb_cst5;*	1			
		3.66: qb_1lce;*	1			
		3.67: qb_cst3;*	1			
		3.68: qb_cst4;*	1			
		3.69: qb_cst5;*	1			
		3.70: qb_1lce;*	1			
		3.71: qb_cst3;*	1			
		3.72: qb_cst4;*	1			
		3.73: qb_cst5;*	1			
		3.74: qb_1lce;*	1			
		3.75: qb_cst3;*	1			
		3.76: qb_cst4;*	1			
		3.77: qb_cst5;*	1			
		3.78: qb_1lce;*	1			
		3.79: qb_cst3;*	1			
		3.80: qb_cst4;*	1			
		3.81: qb_cst5;*	1			
		3.82: qb_1lce;*	1			
		3.83: qb_cst3;*	1			
		3.84: qb_cst4;*	1			
		3.85: qb_cst5;*	1			
		3.86: qb_1lce;*	1			
		3.87: qb_cst3;*	1			
		3.88: qb_cst4;*	1			
		3.89: qb_cst5;*	1			
		3.90: qb_1lce;*	1			
		3.91: qb_cst3;*	1			
		3.92: qb_cst4;*	1			
		3.93: qb_cst5;*	1			
		3.94: qb_1lce;*	1			
		3.95: qb_cst3;*	1			
		3.96: qb_cst4;*	1			
		3.97: qb_cst5;*	1			
		3.98: qb_1lce;*	1			
		3.99: qb_cst3;*	1			
		3.100: qb_cst4;*	1			
		3.101: qb_cst5;*	1			
		3.102: qb_1lce;*	1			
		3.103: qb_cst3;*	1			
		3.104: qb_cst4;*	1			
		3.105: qb_cst5;*	1			
		3.106: qb_1lce;*	1			
		3.107: qb_cst3;*	1			
		3.108: qb_cst4;*	1			
		3.109: qb_cst5;*	1			
		3.110: qb_1lce;*	1			
		3.111: qb_cst3;*	1			
		3.112: qb_cst4;*	1			
		3.113: qb_cst5;*	1			
		3.114: qb_1lce;*	1			
		3.115: qb_cst3;*	1			
		3.116: qb_cst4;*	1			
		3.117: qb_cst5;*	1			
		3.118: qb_1lce;*	1			
		3.119: qb_cst3;*	1			
		3.120: qb_cst4;*	1			
		3.121: qb_cst5;*	1			
		3.122: qb_1lce;*	1			
		3.123: qb_cst3;*	1			
		3.124: qb_cst4;*	1			
		3.125: qb_cst5;*	1			
		3.126: qb_1lce;*	1			
		3.127: qb_cst3;*	1			
		3.128: qb_cst4;*	1			
		3.129: qb_cst5;*	1			
		3.130: qb_1lce;*	1			
		3.131: qb_cst3;*	1			
		3.132: qb_cst4;*	1			
		3.133: qb_cst5;*	1			
		3.134: qb_1lce;*	1			
		3.135: qb_cst3;*	1			
		3.136: qb_cst4;*	1			
		3.137: qb_cst5;*	1			
		3.138: qb_1lce;*	1			
		3.139: qb_cst3;*	1			
		3.140: qb_cst4;*	1			
		3.141: qb_cst5;*	1			
		3.142: qb_1lce;*	1			
		3.143: qb_cst3;*	1			
		3.144: qb_cst4;*	1			
		3.145: qb_cst5;*	1			
		3.146: qb_1lce;*	1			
		3.147: qb_cst3;*	1			
		3.148: qb_cst4;*	1			
		3.149: qb_cst5;*	1			
		3.150: qb_1lce;*	1			
		3.151: qb_cst3;*	1			
		3.152: qb_cst4;*	1			
		3.153: qb_cst5;*	1			
		3.154: qb_1lce;*	1			
		3.155: qb_cst3;*	1			
		3.156: qb_cst4;*	1			
		3.157: qb_cst5;*	1			
		3.158: qb_1lce;*	1			
		3.159: qb_cst3;*	1			
		3.160: qb_cst4;*	1			
		3.161: qb_cst5;*	1			
		3.162: qb_1lce;*	1			
		3.163: qb_cst3;*	1			
		3.164: qb_cst4;*	1			
		3.165: qb_cst5;*	1			
		3.166: qb_1lce;*	1			

ORIGIN						
Query	Match	0.48	Score 27.8;	DB 14;	Length 58;	
Best Local Similarity	65.5%	Pred. No. 2	8e+04;			
Matches	38;	Conservative	0;	Mismatches 20;	Indels 0;	Gaps 0.
QTY	2675	CCATTCTTAAACGAACTGAACTTCAACCAGAGACAGACGCTACTGGCCAAATTA	2732			
DB	1	CCNTTTTACGAGGAGAGATTTTAACTTAAAGAGATTTAAGTNAATTGTCAGGTTCAAGGTTCA	58			
RESULT 2						
BH623868	BH623868	1007097F03 2E1, x1 1007 -	58 bp	DNA linear	GSS 30-JAN-2002	
LOCUS		ResequMu Grid H 2.ea may's genomic, DNA sequence.				
DEFINITION		BH623868				
ACCESSION		BH623868.1	C1:1843719			
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC						
Zea mays						

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 clade; Panicoideae; Andropogonaceae; Zea.  
 1 (bases 1 to 58)  
 Walbot, V  
 Maize genomic sequences found using engineered RescueMu transposon  
 Unpublished (2001)  
 contact: Walbot, V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave., Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221

Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different enzymes  
 Reverse complemented post ligation sequence from source  
 File: 100197 row: 19  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..58  
 "zea mays"  
 "mixed background W23/A188/B73"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone.lib="1007 - RescueMu Grid II"



Query Match Score 0.9%; Score 25.6; DR 14; Length 59;  
Rest Local Similarity 65.4%; Pred. No. 1e-05; Db 54  
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
LOCUS 55 bp mRNA Linear EST 11-JUN-2001  
DEFINITION ax39d04\_x1 Proliferating Human Erythroid Cells (ICB:ax library)  
ACCESSION BG943565  
VERSION BG943565.1 GI:14342937  
KEYWORDS EST.  
ORGANISM Homo sapiens  
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 55)  
AUTHORS Gubin,A.N.,Njoroge,T.M.,Rouffard,G.G. and Miller,J.L.  
TITLE Gene expression in proliferating human erythroid cells  
JOURNAL Genomics 59 (2), 168-177 (1999)  
COMMENT Contact: Jeffrey L. Miller  
Laboratory of Chemical Biology  
National Institute of Diabetes and Digestive and Kidney Diseases  
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD  
Tel: 301 402 2373  
Fax: 301 435 5148  
Email: jml@nih.gov  
DNA Sequencing and analyses by National Institutes of Health  
Intramural Sequencing Center (NIISC).  
Plate: 39 row: d column: 04  
Seq primer: -21M13 forward primer (ABI).  
FEATURES Location/Qualifiers  
1. .55  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="ax39d04"  
/clone\_lib="proliferating Human Erythroid Cells (ICB:ax  
library)"  
/sex="unknown"  
/tissue\_type="blood"  
/cell\_type="Erythroid Cells"  
/cell\_line="Primary Culture of Peripheral Blood  
Mononuclear Cells"  
/dev\_stage="Progenitor: EPO responsive CD71+++"  
/lab\_host="SOLP"  
/note="Organ: blood; Vector: Lambda ZAP II; Site:1: EcoRI;  
Site:2: PstI; RFLP: 65, 610 Proliferating erythroid cells from  
the buffy coat of a blood donor were obtained by flow  
cytometric separation after a 5-day culture period in the  
presence of erythropoietin. Total RNA was purified from  
the sorted cell population using TRIZOL reagent. RNA (0.3  
ug) was converted into double stranded cDNA using  
Clontech's Cappuccin DNA Library Construction Kit  
(Clontech) according to the manufacturer's protocol and  
cloned into EcoRI digested lambda ZAP II vector  
(Stratagene). The phage library was amplified once prior  
to in vivo excision in SOLP cells. Individual colonies  
were grown, and the cDNA inserts were sequenced in high  
throughput (NIH intramural sequencing center  
<http://www.niisc.nih.gov/>)." BASE COUNT 8 a  
ORIGIN

Query Match Score 0.9%; Score 25.2; DR 13; Length 55;  
Rest Local Similarity 66.7%; Pred. No. 1.2e-05; Db 48  
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
LOCUS 60 bp mRNA Linear EST 13-APR-1999  
DEFINITION t995b12\_x1 NC1\_CGAP\_CLL Human Sapiens cDNA clone IMAGE:216511\_3  
similar to gb:X7025\_rna1 INSULIN-LIKE GROWTH FACTOR 1A PRECURSOR

RESULT 7  
AA417159/c  
LOCUS AM417159  
DEFINITION zu13a02\_r1 Soares testis\_NHU Homo sapiens cDNA clone IMAGE:741690  
5' similar to gb:X57025 insulin-like growth factor IA precursor (HUMAN); mRNA sequence.  
ACCESSION AA417159  
VERSION AA417159.1 GI:2077240  
KEYWORDS EST.  
SOURCE Human.  
ORGANISM Homo sapiens  
REFERENCE Fukuyama, Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
AUTHORS Billier,L., Allen,M., Bowles,L., Dubuque,T., Geissel,G., Josi,S.,  
Kucaba,T., Lacy,M., Le,N., Lemmon,G., Marra,M., Martin,J., Moore,B.,  
Schellingerq,K., Steffen,M., Tan,F., Theisius,B., White,Y., Wylie,  
T., Waterston,R. and Wilson,R.  
TITLE WashU-Merck EST project 1997  
JOURNAL Unpublished (1997)  
COMMENT Contact: Wilson BR  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL : contact the  
IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
Trace considered overall poor quality  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 1.  
FEATURES Source  
1. .51  
/organism="Homo sapiens"  
/db\_xref="GDB:5928756"  
/db\_xref="taxon:9606"  
/clone="IMAGE:731690"  
/clone\_lib="Soares\_testis\_NHU"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D Pac (Pharmacia) with a modified  
poly linker; Site:1: Not I, Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
Inc. and primed with a Not I (5'-GGGTCT) primer [5'-  
TGTTACCAATTCTAACATGCCAGCGCCCATTTTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7Z vector. Library  
went through one round of normalization to cDNA, and was  
constructed by Bent Soares and M. Fatima Bonaldo." BASE COUNT 10 a  
ORIGIN 18 c 7 q 16 t

RESULT 8  
AA523624  
LOCUS AM523624  
DEFINITION 60 bp mRNA Linear EST 13-APR-1999



/clone="IMAGE:4950911"  
 /clone.lib="NCI\_CGAP\_Mam6"  
 /sex="female"; virgin"  
 /issue\_type="infiltrating ductal carcinoma"  
 /dev\_stage="5 months"  
 /lab\_host="PHL08"  
 /tissue="Ovary; mammary, Vector; PCMV SV40; Site\_1: Salit;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies, Investigator:  
 Providing samples: Jeffrey Green, M.D., NIH"  
 BASE COUNT 37 a 1 c 9 q 13 t  
 ORIGIN

Query Match 0.8%; Score 24; DB 13; length 60;  
 Best Local Similarity 64.3%; Prej No. 2 6e+05;  
 Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2105 AATTCGGAGAACATTCGAAAGATAAAAGATCAAATTAACATTCC 2160  
 Db 4 ATTTGAAAGTAAATATTTCGAAACAAAAAGAAAAAAGAAAAAGG 59

RESULT 11  
 BG671284 HG671284 54 bp mRNA Linear EST 30-APR-2001  
 LOCUS DRNBOA12 Rat DRG 1 library Rattus norvegicus cDNA clone DRNBOA12 5' ,  
 DEFINITION mRNA sequence.  
 ACCESSION BG671284  
 VERSION BG671284.1 GI:13893383  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 54)  
 AUTHORS Xian, Huang, Q. H., Zhang, F. X., Bac, I., Lu, Y. J., Guo, C., Yang, L.,  
 Huang, W. J., Fu, G., Xu, S. H., Cheng, X. P., Yan, Q., Zhu, Z. D., Zhang,  
 X., Chen, Z., Han, Z. G. and Zhang, X.  
 TITLE Identification of gene expression profile of dorsal root ganglion  
 in the rat peripheral axotomy model of neuropathic pain  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
 MEDLINE 22056133  
 COMMENT Contact: Zhang Xu  
 Laboratory of Sensory System  
 Institute of Neuroscience  
 320 Yue Yang Road, Shanghai 200031, P.R.China  
 Tel: 86-21-64148700-121  
 Fax: 86-21-64713446  
 Email: xu\_zhang@ion.ac.cn  
 This clone is also available at Chinese National Human Genome  
 Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
 Pudong New Area, P.R.China. Please contact with Zhang Xu  
 (xu\_zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)  
 PCR PRIMERS  
 FORWARD: T3  
 BACKWARD: T7  
 Seq Drimer: T3  
 POLY-A-NO.

FEATURES SOURCE  
 Location/Qualifiers 1..54  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="DRGNB0A12"  
 /clone\_lib="Rat DRG Library"  
 /sex="male"  
 /issue\_type="dorsal root ganglion"  
 /dev\_stage="adult"  
 /note="Total RNA was isolated from hypothalamus and  
 transcribed into cDNA, which was then used as template in  
 PCR. The PCR products were separated on sequencing gel.  
 The different bands were cut, reamplified, cloned into

BASE COUNT 33 a 2 c 6 g 13 t  
 ORIGIN

Query Match 0.8%; Score 23.8; DB 12; length 54;  
 Best Local Similarity 80.0%; Prej. No. 2.8e+05;  
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2006 AGATATTAGATGTGTTATGAANANANGATAA 2040  
 Db 14 AAGTATATTGAAATGTGATGAAAAA 48

RESULT 12  
 BI246744 BI246744 59 bp mRNA Linear EST 17-JUL-2001  
 LOCUS K02949667F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:5125241 5'  
 DEFINITION mRNA sequence.  
 ACCESSION BI246744  
 VERSION BI246744.1 GI:14791003  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus  
 (bases 1 to 59)  
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/  
 Unpublished (MGC)  
 Contact: Robert Strausberg, ph.d.  
 Email: cgaps-r@mail.nih.gov  
 Tissue procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The IMAGE Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the IMAGE Consortium/LIN, at:  
 http://image.llnl.gov/  
 Plate: LLAM1306 row: e column: 18  
 High quality sequence stop: 59.  
 FEATURES Source  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5125241"  
 /clone.lib="NCI\_CGAP\_Li9"  
 /lab\_host="D1010 (T1 phage resistant)"  
 /note="Organ: liver; Vector: pCMV-Sp6Kb; site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; primer: Oligo dT  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCI-CGAP Library."  
 BASE COUNT 17 a 17 q 10 t  
 ORIGIN

Query Match 0.8%; Score 23.8; DB 13; length 59;  
 Best Local Similarity 72.1%; Prej. No. 2 9e+05;  
 Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2687 TGAGGAACCTGAGACTCAGAGACTGTGACTGCTACTGCCAAACA 2729  
 Db 3 TAGGAAACCTGGGCTCACAGAGCTTCACTTGTCAGTCAGAA 45

RESULT 13  
 BI148041 BI148041 60 bp mRNA Linear EST 05-JUL-2001  
 LOCUS 60291557F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:5053555 5'  
 DEFINITION mRNA sequence.  
 ACCESSION BI148041  
 VERSION BI148041.1 GI:14608042  
 KEYWORDS EST.  
 SOURCE house mouse.



Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
Qy 2864 TCTCATTCATTCATTCAGTATTGACATCTAGATAAGTC 2907  
Db 3 TTTTTTCAACAGCTTATGAGCTACTCTGCC 46

Search completed: April 17, 2003, 02:29:52  
Job time : 4485 secs

Minimum DB seq length: 0  
 Maximum DB seq length: 60

Post processing: Minimum Match 0.8  
 Maximum Match 100%

Listing first 45 summaries

Database:	Issued_Patents_NA,*
1:	/eqn2_6/podata/1/irna/5A_COMB.seq;*
2:	/eqn2_6/podata/1/irna/5B_COMB.seq;*
3:	/eqn2_6/podata/1/irna/6A_COMB.seq;*
4:	/eqn2_6/podata/1/irna/6B_COMB.seq;*
5:	/eqn2_6/podata/1/irna/petunia_COMB.seq;*
6:	/eqn2_6/podata/1/irna/backtail1.seq;*

Total number of hits satisfying chosen parameters: 645134

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	4.9-4	1-7	51	4	US 08-973-005A-4	Sequence 4, Appli	
2	4.5	1-2	35	4	US 08-973-005A-7	Sequence 7, Appli	
3	4.5	1-2	35	4	US 08-973-005A-H	Sequence 8, Appli	
4	2.5	0-9	48	1	US 08-783-275-6	Sequence 6, Appli	
5	2.5	0-9	48	1	US 08-277-708-6	Sequence 6, Appli	
6	2.3	0-9	54	2	US 08-418-048N-71	Sequence 7, Appli	
7	2.2-6	0-8	47	1	US 08-867-106-6	Sequence 6, Appli	
8	2.2-4	0-8	60	4	US 09-284-627-14	Sequence 14, Appli	
9	2.2-2	0-8	60	4	US 09-044-888A-7	Sequence 7, Appli	
10	2.1-8	0-7	39	4	US 09-079-984A-9	Sequence 9, Appli	
11	2.1-6	0-7	47	4	US 09-641-638-710	Sequence 70, Appli	
12	2.1-6	0-7	51	1	US 08-379-926A-2	Sequence 2, Appli	
13	2.1-6	0-7	51	1	US 08-484-415-21	Sequence 3, Appli	
14	2.0-6	0-7	45	1	US 08-484-415-21	Sequence 21, Appli	
15	2.0-6	0-7	60	2	US 08-464-257-9	Sequence 9, Appli	
16	2.0-6	0-7	60	2	US 08-362-375-9	Sequence 9, Appli	
17	2.0-4	0-7	60	3	US 09-203-796A-9	Sequence 9, Appli	
18	2.0-8	0-7	59	4	US 09-542-646-12	Sequence 12, Appli	
19	2.0-6	0-7	60	4	US 09-088-086-12	Sequence 12, Appli	
20	2.0-6	0-7	45	6	6487983-18	Patent No. 5487983	
21	2.0-6	0-7	54	4	US 09-711-62B-7	Sequence 7, Appli	
22	2.0-6	0-7	54	4	US 09-171-62B-8	Sequence 8, Appli	
23	2.0-2	0-7	57	4	US 09-609-816-12	Sequence 12, Appli	
24	2.0-2	0-7	46	4	US 09-406-074-3	Sequence 3, Appli	
25	2.0-2	0-7	47	4	US 09-641-638-728	Sequence 758, Appli	
26	2.0-2	0-7	51	4	US 09-358-972-211	Sequence 21, Appli	
27	2.0-2	0-7	51	4	US 09-430-615-21	Sequence 21, Appli	

Copyright (c) 1993 - 2003 Compugen Ltd.  
**nm** nucleic nucleic search, using sw model  
Run on: Apri 11 16, 2004, 22:43:09 : Search time 111 Seconds  
(without alignments)  
8089.636 Million cell updates/sec

Title: US 09-954 679 3  
 Perfect Score: 2928  
 Sequence: 1. atcccaactacactaaa.....ggcactggatcatgaaatt 2928

Scoring table: IDENTITY NUC gapop 10.0 Gapext 1.0

Searched: 441362 seqs, 15338381 residues

RESULT 1  
 US 08-973-005A-4  
 Sequence 4, Application US/08973-005A  
 Patent No. 6420099

GENERAL INFORMATION

APPLICANT: ISHIDA, Isao  
 YOSHIOKA, Masaharu  
 ISHIDA, Isao

TITLE OF INVENTION: VIRUS RESISTANT PLANTS EXPRESSION ANIMAL CELL DERIVED (Z'') ALIGMENTENYLATE SYNTHETASE AND RIBONUCLEASE L AND A METHOD FOR CREATING THE SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner  
 STREET: 4000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-3109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/Windows  
 CURRENT APPLICATION DATA:

SOFTWARE: Patent in Reissue #1.0, Version #1.00  
 APPLICATION NUMBER: US2009/02973-005A  
 FILING DATE: 01 Dec 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 11-074-1/1994  
 FILING DATE: 31-May 1995  
 APPLICATION NUMBER: JP 12-0401/1995  
 FILING DATE: 01-Nov 1995  
 APPLICATION NUMBER: JP 5-2010/1995  
 FILING DATE: 08 Mar 1996

ATTORNEY/AGENT INFORMATION:

NAME: Bentz, Stephen A.  
 REGISTRATION NUMBER: 29-7768

REFERENCE/LOCATED NUMBER: 081346/01114

TELECOMMUNICATION INFORMATION:

TELE-REF: (202)622-5300  
 TELEFAX: (202)622-5399

TELEX: 904146

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 51 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear

MISCELLANEOUS INFORMATION:

DESCRIPTION: /desc - synthetic RNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

us-08-973-005A-4

Query Match      1.7%    Score 49.4; DB 4;    Length 51;

Best Local Similarity 98.0%;    Pred. No. 1.Ac-05;

Matches 50;    Conservative 0;    Mismatches 0;    Gaps 0;

Qy    374 AATGAGGTTTACGTTTATGATTCGGTAAAGAAATTGAAATTG 424

Db    1 AATGGGCCACCCGTTTATCCCTCGCAGTTCGGGAGCTGAAGCTG 51

RESULT 2

; Sequence 7, Application US/08973005A

; Patent No. 6320099

; GENERAL INFORMATION:

;    APPLICANT: OGAWA Toshiya

;    ADDRESS: YOSHIOKA Massaharu

;    CITY: ISHIDA Isao

;    NUMBER OF SEQUENCES: 12

;    CORRESPONDENCE ADDRESS:

;    ADDRESS: Foley & Lardner

;    STREET: 3000 K Street, N.W., Suite 500

;    CITY: Washington

;    STATE: D.C.

;    ZIP: 20007-5109

;    COMPUTER READABLE FORM:

;    MEDIUM TYPE: Floppy disk

;    COMPUTER: IBM PC compatible

;    OPERATING SYSTEM: PC-DOS/MS-DOS

;    SOFTWARE: Patent In Release #1.0, Version #1.30

;    CURRENT APPLICATION DATA:

;    APPLICATION NUMBER: US/08/973,005A

;    FILING DATE: 01-Dec-1997

;    PRIORITY APPLICATION DATA:

;    APPLICATION NUMBER: JP 133741/1995

;    FILING DATE: 31-MAY-1995

;    APPLICATION NUMBER: JP 285401/1995

;    FILING DATE: 01-NOV-1995

;    APPLICATION NUMBER: JP 5,2010/1995

;    FILING DATE: 01-Dec-1997

;    ATTORNEY/AGENT INFORMATION:

;    NAME: Bent, Stephen A.

;    REGISTRATION NUMBER: 29,768

;    REFERENCE/POCKET NUMBER: 081356/0113

;    TELECOMMUNICATION INFORMATION:

;    TELEPHONE: (202)267-5300

;    TELEX: 904136

;    INFORMATION FOR SEQ ID NO: 8:

;    SEQUENCE CHARACTERISTICS:

;    LENGTH: 35 base pairs

;    TYPE: nucleic acid

;    STRANDEDNESS: single

;    TOPOLOGY: linear

;    MOLECULE TYPE: other nucleic acid

;    DESCRIPTION: /desc = "synthetic DNA"

;    SEQUENCE DESCRIPTION: SEQ ID NO: 8:

us-08-973-005A-8

RESULT 4

us-08-783-275-6

; Sequence 6, Application US/08783275

; Patent No. 5766899

; GENERAL INFORMATION:

;    APPLICANT: Vojdani, Aristo

;    ADDRESS: Mordechai, Eli

;    TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS

;    TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROME

;    NUMBER OF SEQUENCES: 8

;    RESULT 3

us-08-973-005A-4

;    Sequence 8, Application US/08973005A

;    Patent No. 6320099

;    GENERAL INFORMATION:

;    APPLICANT: OGAWA Toshiya

;    ADDRESS: YOSHIOKA Massaharu

;    CITY: ISHIDA Isao

;    NUMBER OF SEQUENCES: 12

;    CORRESPONDENCE ADDRESS:

;    ADDRESS: Foley & Lardner

;    STREET: 3000 K Street, N.W., Suite 500

;    CITY: Washington

;    STATE: D.C.

;    ZIP: 20007-5109

;    COMPUTER READABLE FORM:

;    MEDIUM TYPE: Floppy disk

;    COMPUTER: IBM PC compatible

;    OPERATING SYSTEM: PC-DOS/MS-DOS

;    SOFTWARE: Patent In Release #1.0, Version #1.30

;    CURRENT APPLICATION DATA:

;    APPLICATION NUMBER: US/08/973,005A

;    FILING DATE: 01-Dec-1997

;    PRIORITY APPLICATION DATA:

;    APPLICATION NUMBER: JP 133741/1995

;    FILING DATE: 31-MAY-1995

;    APPLICATION NUMBER: JP 285401/1995

;    FILING DATE: 01-NOV-1995

;    APPLICATION NUMBER: JP 5,2010/1995

;    FILING DATE: 01-Mar-1996

;    ATTORNEY/AGENT INFORMATION:

;    NAME: Bent, Stephen A.

;    REGISTRATION NUMBER: 29,768

;    REFERENCE/POCKET NUMBER: 081356/0113

;    TELECOMMUNICATION INFORMATION:

;    TELEPHONE: (202)267-5300

;    TELEX: 904136

;    INFORMATION FOR SEQ ID NO: 8:

;    SEQUENCE CHARACTERISTICS:

;    LENGTH: 35 base pairs

;    TYPE: nucleic acid

;    STRANDEDNESS: single

;    TOPOLOGY: linear

;    MOLECULE TYPE: other nucleic acid

;    DESCRIPTION: /desc = "synthetic DNA"

;    SEQUENCE DESCRIPTION: SEQ ID NO: 8:

us-08-973-005A-8

;    RESULT 4

us-08-783-275-6

; Sequence 6, Application US/08783275

; Patent No. 5766899

; GENERAL INFORMATION:

;    APPLICANT: Vojdani, Aristo

;    ADDRESS: Mordechai, Eli

;    TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS

;    TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROME

;    NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92660

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSHQ Version 1.5

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/783,275  
 FILING DATE: 16 JAN 1997  
 CLASSIFICATION: 445

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/727,708  
 FILING DATE: 16 JAN 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barteldt, Neil S.  
 REFERENCE/DOCKET NUMBER: 49,901  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619 235 8550  
 TELEFAX: 619 235 0176  
 TELEX:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 48 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear

RESULT 5  
 US 08/727,708 6  
 Sequence 6, Application US/08/727,708  
 Patent No. 5,766,900  
 GENERAL INFORMATION:  
 APPLICANT: Yoshida, Atsuto  
 APPLICANT: Modedchai, Eli  
 TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS  
 TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROM  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92660

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/418,849  
 FILING DATE: 07 Aug 1995  
 CLASSIFICATION: 546  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/946,849  
 FILING DATE: 28 Aug 1992  
 CLASSIFICATION: 546  
 ATTORNEY/AGENT INFORMATION:  
 NAME: RICHARD W. IRK  
 REFERENCE/DOCKET NUMBER: 16,449  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 758 4800  
 TELEFAX: 212 751 6849  
 TELEX: 421792

SEQUENCE CHARACTERISTICS:  
 LENGTH: 64 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US 08/418,849 71

FILING DATE: 07 Aug 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barteldt, Neil S.  
 REFERENCE/DOCKET NUMBER: 49,901  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619 235 8550  
 TELEFAX: 619 235 0176  
 TELEX:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 48 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear

RESULT 6  
 US 08/418,849 71/C  
 Sequence 71, Application US/08/16848A  
 Patent No. 5,847,046  
 GENERAL INFORMATION:  
 APPLICANT: SCHERFELD, MANFRED, HARMISON, L.,  
 APPLICANT: GEORGE G., CHANG JIE, CHEN, HANTEK, FA, AKEU  
 TITLE OF INVENTION: INFFECTIVE, INTERFERING,  
 HIV PARTICLES  
 NUMBER OF SEQUENCES: 77  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
 STREET: 445 PARK AVENUE  
 CITY: NEW YORK  
 COUNTRY: U.S.A.  
 ZIP: 10016  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/08/418,849  
 FILING DATE: 07 Aug 1995  
 CLASSIFICATION: 546  
 ATTORNEY/AGENT INFORMATION:  
 NAME: RICHARD W. IRK  
 REFERENCE/DOCKET NUMBER: 16,449  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 758 4800  
 TELEFAX: 212 751 6849  
 TELEX: 421792

SEQUENCE CHARACTERISTICS:  
 LENGTH: 64 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

Query Match Score 25: DB 1; Length 48:  
 Host Local Similarity 100.0%; Pred. No. 44,02;  
 Matches 25; conservative; 0; Mismatches 0; Gaps 0;  
 Gaps 0;

QY 638 GGACAGTGTGGTCGAAATT 66,2  
 Ob 1 GGACAGTGTGGTCGAAATT 25

Query Match Score 25: DB 1; Length 48:  
 Host Local Similarity 100.0%; Pred. No. 44,02;  
 Matches 25; conservative; 0; Mismatches 0; Gaps 0;  
 Gaps 0;

QY 638 GGACAGTGTGGTCGAAATT 66,2  
 Ob 1 GGACAGTGTGGTCGAAATT 25



RESULT 10  
OS 09 079 984 9/  
2 Sequence: 9; Application US/19079484  
2 Patent No. 6,241,810

GENERAL INFORMATION:

2 APPLICANT: Okano, Fumiyoshi, Satoshi, Massahiro,  
2 TITLE OF INVENTION: Canine interleukin 12, a production method  
2 and thereof, an immune disease treatment method and preventive  
2 TITLE OF INVENTION: method using it  
2 NUMBER OF SEQUENCES: 16  
2 CORRESPONDENCE ADDRESS:  
2 ADDRESSEE: Miller & Christenbury intellectual property  
2 ADDRESS: Department of Schmader, Harrison, Segal and Lewis, LLP  
2 STREET: 1600 Market Street, 39th Floor  
2 CITY: Philadelphia  
2 STATE: PA  
2 COUNTRY: USA  
2 ZIP: 19104

COMPUTER READABLE FORM:

2 MEDIUM TYPE: Floppy disk  
2 COMPUTER: IBM PC compatible  
2 OPERATING SYSTEM: pc dos/MS dos  
2 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

2 APPLICATION NUMBER: US/09/079/984A  
2 FILING DATE: 15 MAY 1998  
2 ATTORNEY/AGENT INFORMATION:  
2 NAME: Austin R. Miller  
2 REGISTRATION NUMBER: 16,602  
2 REFERENCE/DOCKET NUMBER: 1051-98  
2 TELEPHONE: (215) 563-1810  
2 TELEFAX: (215) 568-6946  
2 INFORMATION FOR SEQ ID NO: 9:  
2 SEQUENCE CHARACTERISTICS:  
2 LENGTH: 49 bases  
2 TYPE: nucleic acid  
2 STRANDEDNESS: single  
2 TOPOLOGY: linear  
2 Molecule TYPE: other DNA; synthetic DNA  
OS 09 079 984 9

Query Match 0.78; Score 21.8; DB 4; Length 39;  
2 best local similarity 78.8%; Pred. No. 2, Bev.03;  
2 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 11  
OS 09 641 648 770  
2 Sequence: 770; Application US/09641638

GENERAL INFORMATION:

2 APPLICANT: Blumenteld, Marta  
2 APPLICANT: Boudeleter, Lydie  
2 APPLICANT: Cohen, Annick  
2 TITLE OF INVENTION: BIULLETIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
2 FILE REFERENCE: GENSET/ICP  
2 CURRENT APPLICATION NUMBER: US/09/641,638  
2 CURRENT FILING DATE: 2000-08-16  
2 PRIORITY FILING DATE: 2000-02-11  
2 PRIORITY APPLICATION NUMBER: US 60/133,230  
2 PRIORITY FILING DATE: 1999-05-07  
2 PRIORITY APPLICATION NUMBER: US 09/275,267

RESULT 12  
US 08-319-926A-2/Z  
2 Sequence 2, Application US/08179926A  
2 Patent No. 5,784,114

GENERAL INFORMATION:

2 APPLICANT: GARREZ, DIRK  
2 APPLICANT: ROSS, JOEL  
2 TITLE OF INVENTION: EXPRESSION SYSTEM, INTEGRATION  
2 TITLE OF INVENTION: VECTOR  
2 NUMBER OF SEQUENCES: 8  
2 CORRESPONDENCE ADDRESS:  
2 ADDRESSEE: NEUSTADT, SPIVAK, MCCLELLAND, MILLER &  
2 STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400  
2 CITY: ALEXINGTON  
2 STATE: VA  
2 COUNTRY: USA  
2 ZIP: 22202

COMPUTER READABLE FORM:

2 MEDIUM TYPE: Floppy disk  
2 COMPUTER: IBM PC compatible  
2 OPERATING SYSTEM: PC-DOS/MS DOS  
2 SOFTWARE: Patent In Release #1.0, Version #1.40  
2 CURRENT APPLICATION DATA:  
2 APPLICATION NUMBER: US/08/319,926A  
2 FILING DATE: 27-JAN-1995  
2 CLASSIFICATION: 435  
2 PRIOR APPLICATION DATA:  
2 APPLICATION NUMBER: BE 094/00102  
2 FILING DATE: 28 JAN 1994  
2 PRIOR APPLICATION DATA:  
2 APPLICATION NUMBER: BE 094/00586  
2 FILING DATE: 17-JUN 1994  
2 PRIOR APPLICATION DATA:  
2 APPLICATION NUMBER: BE 095/0014  
2 FILING DATE: 09-JAN-1995  
2 ATTORNEY/AGENT INFORMATION:  
2 NAME: OBACION, NORMAN F  
2 REGISTRATION NUMBER: 24,618  
2 REFERENCE/DOCKET NUMBER: 3487 1-0  
2 TELECOMMUNICATION INFORMATION:  
2 TELEPHONE: 704-413-4000  
2 TELEFAX: 704-413-2220  
2 TELEX: 248855 OPAT OR  
2 INFORMATION FOR SEQ ID NO: 2:  
2 Sequence CHARACTERISTICS:  
2 LENGTH: 61 base pairs  
2 TYPE: nucleic acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "synthetic oligonucleotide"  
 US-08-379-926A-2

Query Match Similarity 0.7%; Score 21.6; DB 1; Length 51;  
 Best Local Similarity 68.2%; Pred. No. 3, Re+03;  
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

US-08-379-926A-3/c  
 Sequence 3, Application US/08379926A  
 Patent No. 5783414

GENERAL INFORMATION:  
 APPLICANT: ROOS, JOEL  
 TITLE OF INVENTION: EXPRESSION SYSTEM, INTEGRATION  
 TITLE OF INVENTION: VECTOR  
 TITLE OF INVENTION: AND CELL TRANSFORMED BY THIS INTEGRATION VECTOR  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCULLAGH, MAIER &  
 ADDRESS: NEUSTADT  
 STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/379, 926A  
 FILING DATE: 27-JAN-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: BE 094 00102  
 FILING DATE: 28-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: BE 094 00586  
 FILING DATE: 17-JUN-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: BE 095 00014  
 FILING DATE: 09-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F  
 REGISTRATION NUMBER: 24, 618  
 REFERENCE/DOCKET NUMBER: 3987-13-0

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 51 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "synthetic oligonucleotide"  
 US-08-379-926A-3

Query Match Similarity 0.7%; Score 21.6; DB 1; Length 51;  
 Best Local Similarity 68.2%; Pred. No. 3, Re+03;  
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Query 2524 AACCTTACCAACTAACGAGCACATCGTAAGATCCTT 2567  
 Sequence 9, Application US/08464257  
 Patent No. 5830707

GENERAL INFORMATION:  
 APPLICANT: Bushman, Frederic D.  
 TITLE OF INVENTION: METHOD FOR SITE-SPECIFIC INTEGRATION OF  
 TITLE OF INVENTION: NUCLEAR ACTIVITIES AND RELATED PRODUCTS  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
 STREET: 444 South Flower Street, Suite 2000  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: pro-POS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464, 257  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ramos, Robert T.  
 REGISTRATION NUMBER: 37, 915  
 REFERENCE/DOCKET NUMBER: P41 9993  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-546-1995  
 TELEX: 619-546-9392  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 60 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: Oligonucleotide

US-08-444-257-9  
 Query Match Similarity 0.7%; Score 21; DB 2; Length 60;  
 Best Local Similarity 62.3%; Pred. No. 6, 5e+03;  
 Matches 33; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 DB 1740 GAAATGAGGAGCTTCACATTCAGATCAAGACCCATT 1792  
 Query 1740 GAAATGAGGAGCTTCACATTCAGATCAAGACCCATT 1792  
 Sequence 9, Application US/084642375  
 Patent No. 5916804

GENERAL INFORMATION:  
 APPLICANT: Bushman, Frederic D.  
 TITLE OF INVENTION: METHOD FOR SITE-SPECIFIC INTEGRATION OF  
 TITLE OF INVENTION: NUCLEAR ACTIVITIES AND RELATED PRODUCTS  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
 STREET: 444 South Flower Street, Suite 2000  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90071  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER SYSTEM: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/062,375  
 FILING DATE: 05 JUN 1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/464,257  
 FILING DATE: 05 JUN 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ramos, Robert T.  
 REGISTRATION NUMBER: 37,915  
 REFERENCE/DOCKET NUMBER: P41 999-8  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-546-9495  
 TELEFAX: 619-546-9492  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 60 base pairs  
 TYPE: nucleic acid  
 STANDALONE: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: oligonucleotide  
 US 09 062 375 9

Query Match 0.7% Score 21; DB 2; Length 60;  
 Best Local Similarity 62.8% Pred. No. 6.5e+03;  
 Matches 44; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1740 GTTATGAAAGGGTGTTCAGTTCTAGATGAGAACTTAAGGACCTATT 1792  
 14b 7 GGAATAGAAAGTACTAACTTCCGAGATGAGCACAAAAAGAACCAAT 59

Search completed: April 17, 2003, 04:30:22  
 Job time: 1.26 secs

